

1 GCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT
 51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GAACTGGCTT
 101 CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG
 151 GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA
 201 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG
 251 GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA
 301 CGGGGGGTTT GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA
 351 CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG
 401 GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC
 451 GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCTGTG
 501 GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTGTGAT GCTCGTCAGG
 551 GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCCGAATTA CCGCGGTCTT
 601 TCTCAACGTA ACACTTTACA GCGGCGCGTC ATTTGATATG ATGCGCCCCG
 651 CTTCCCGATA AGGGAGCAGG CCAGTAAAAG CATTACCCGT GGTGGGGTTC
 701 CCGAGCGGCC AAAGGGAGCA GACTCTAAAT CTGCCGTCAT CGACTTCGAA
 751 GGTTCAATC CTTCCCCAC CACCATCACT TTCAAAAGTC CGAAAGAATC
 801 TGCTCCCTGC TTGTGTGTTG GAGGTCGCTG AGTAGTGGC GAGTAAATTT
 851 TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGCATGA AGAATCTGCT
 901 TAGGGTTAGG CGTTTTGCGC TGCTTCGCGA TGTACGGGCC AGATATACCG
 951 GTTGACATTG ATTATTGACT AGTTATTAAT AGTAATCAAT TACGGGGTCA
 1001 TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAAA
 1051 TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG ACGTCAATAA
 1101 TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA
 1151 TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA
 1201 TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC
 1251 CCTGGCATTG TGCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG
 1301 TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC GGTTTTGGCA
 1351 GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC
 1401 TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG
 1451 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG
 1501 AATTCCTGGG CGGGACTGGG GAGTGGCGAG CCCTCAGATG CTGCATATAA
 1551 GCAGCTGCTT TTTGCCTGTA CTGGGTCTCT CTGGTTAGAC CAGATCTGAG
 1601 CCTGGGAGCT CTCTGGCTAA CTAGAGAACC CACTGCTTAA GCCTCAATAA
 1651 AGCTTCTAGA GATCCCTCGA CCTCGAGGGA TCTTCATAC CTACCAGTTC

FIG. 1A

Out
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1701 TCGCCTGCA GGTCCGGCC GCGACTCTAG AGGATCTTTG TGAAGGAACC
1751 TTA CTCTGT GGTGTGACAT AATTGGACAA ACTACCTACA GAGATTTAAA
1801 GCTCTAAGGT AAATATAAAA TTTTAAAGTG TATAATGTGT TAACTACTG
1851 ATTCTAATTG TTTGTGTATT TTAGATTCCA ACCTATGGAA CTGATGAATG
1901 GGAGCAGTGG TGAATGCCT TTAATGAGGA AAACCTGTTT TGCTCAGAAG
1951 AAATGCCATC TAGTGATGAT GAGGCTACTG CTGACTCTCA ACATTCTACT
2001 CCTCCAAAAA AGAAGAGAAA GGTAGAAGAC CCCAAGGACT TTCCTTCAGA
2051 ATTGCTAAGT TTTTGTAGTC ATGCTGTGTT TAGTAATAGA ACTCTTGCTT
2101 GCTTTGCTAT TTACACCACA AAGGAAAAAG CTGCACTGCT ATACAAGAAA
2151 ATTATGGAAA AATATTCTGT AACCTTTATA AGTAGGCATA ACAGTTATAA
2201 TCATAACATA CTGTTTTTTC TTA CTCCACA CAGGCATAGA GTGCTGCTA
2251 TTAATAACTA TGCTCAAAAA TTGTGTACCT TTAGCTTTTT AATTGTAAA
2301 GGGGTTAATA AGGAATATTT GATGTATAGT GCCTTGACTA GAGATCATAA
2351 TCAGCCATAC CACATTTGTA GAGGTTTTAC TTGCTTTAAA AAACCTCCCA
2401 CACCTCCCCC TGAACCTGAA ACATAAAATG AATGCAATTG TTGTTGTAA
2451 CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA
2501 ATTTACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTCC
2551 AAATCATCA ATGTATCTTA TCATGTCTGG ATCCTGTGGA ATGTGTGTCA
2601 GTTAGGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA
2651 GCATGCATCT CAATFAGTCA GCAACCAGGT GTGGAAAGTC CCCAGGCTCC
2701 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT
2751 AGTCCCGCCC CTA ACTCCGC CCATCCCGCC CCTA ACTCCG CCCAGTCCG
2801 CCCATTCTCC GCCCCATGGC TGA CTAA TTTTATTTA TGCAGAGGCC
2851 GAGGCCGCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG GAGGCTTTTT
2901 TGGAGGCCTA GGCTTTTGCA AAAAGCTAAT TC

FIG. 1B

CCTAAGATGAGCTTTCCATGTAAATTTGTAGCCAGCTTCCTTCTGATTTTCAATGTTTCT (60)
 METSERPHEPROCYSLYSPHEVALALASERPHELEULEULEPHEASNVALSER
 TCCAAAGGTGCAGTCTCCAAGAGATTACGAATGCCTTGGAAACCTGGGGTGCCTTGGGT (120)
 SERLYSGLYALAVALSERLYSGLUILETHRASNALALEUGLUTHRTRPGLYALALEUGLY
 20 CAGGACATCAACTTGGACATTCCTAGTTTTCAAATGAGTGATGATATTGACGATATAAAA (180)
 GLNASPILEASNLEUASPILEPROSERPHEGLNMETSERASPPASPILEASPASPILELYS
 TGGGAAAAA¹ACTTCAGACAAGAAAAAGATTGCACAATTCAGAAAAGAGAAAGAGACTTTC (240)
 40 TRPGLULYSTHRSERASPLYSLYSILEALAGLNPH¹EARGLYSGLULYSGLUTHRPH¹E
 AAGGAAAAAGATACATATAAGCTATTTAAAAATGGA¹ACTCTGAAAATTAAGCATCTGAAG (300)
 60 LYSGLULYSASP¹THR¹TYR¹LYS¹LEU¹PH¹ELYS¹ASNGLY¹THR¹LEU¹LYS¹ILE¹LYSHIS¹LEU¹LYS
 ---CHO---
 80 ACCGATGATCAGGATATCTACAAGGTATCAATATATGATACAAAAGGAAAAAATGTGTTG (360)
 THRASPASPGLNASPILETYR¹LYS¹VALSER¹ILE¹TYRASP¹THR¹LYS¹GLY¹LYS¹ASN¹VALLEU
 GAAAAAATAITTTGATTTGAAGATTCAAGAGAGGGTCTCAAAACCAAAGATCTCCTGGACT (420)
 100 GLULYSILEPHEASPLEULYSILEGLNGLUARGVALSERLYSPROLYSILESERTRP¹THR
 TGTATCAACACAACCTGACCTGTGAGGTAAATGAATGGA¹ACTGACCCCGAATTAACCTG (480)
 120 CYSILEASN¹THR¹THR¹LEU¹PH¹RCYS¹GLU¹VALMETASNGLY¹THRASP¹PROGLULEUASN¹LEU
 ---CHO---
 140 TATCAAGATGGGAAACATCTAAAACCTTTCTCAGAGGGTCATCACACACAAGTGGACCAC¹ (540)
 TYRGLNASPGLYLYSHISLEULYSLEUSERGLNARGVALILETHR¹HISLYSTRP¹THR¹THR
 AGCCTGAGTGCAAAATTCAAGTGCACAGCAGGGAACAAAGTCAGCAAGGAATCCAGTGT¹ (600)
 160 SERLEUSERALALYS¹PH¹ELYS¹CYS¹THRALAGLYASNLYSVALSERLYSGLUSERSERVAL
 GAGCCTGTCACTGTCCAGAGAAAGGTCTGGACATCTATCTCATCTTGGCATATGTGGA¹ (660)
 180 GLU¹PROVALSERCYS¹PROGLULYSGLY¹LEU¹ASP¹ILE¹TYR¹LEU¹ILE¹ILEGLY¹ILECYSGLY
 GGAGGCAGCCTCTTGATGGTCTTTGTGGCACTGCTCGTTTTCTATATCACAAAAGGAAA (720)
 200 GLYGLYSERLEULEUMETVALPHEVALALALEULEUVALPHE¹TYR¹ILE¹THR¹LYSARGLYS
 -----TM-----
 220 AAACAGAGGAGTCGGAGAAATGATGAGGAGCTGGAGACAAGAGCCCACAGAGTAGCTACT (780)
 LYSGLNARGSERARGARGASNASPGULGLULEUGLUTHRARGALAHISARGVALALATHR
 GAAGAAAGGGGCCGAAGCCCAACAAATTCAGCTTCAACCCCTCAGAATCCAGCAACT¹ (840)
 240 GLUGLUARGGLYARGLYSPROGLNGLNILEPROALASERTHRPROGLNASNPROALATHR
 TCCCAACATCTCTCCACCACTGGTCA¹TCGTTCCCAAGGCACCTAGTCA¹TCGTC¹CCCCG (900)
 260 SERGLNHISPROPROPROPROGLYHISARGSERGLNALAPROSERHISARGPROPRO
 CCTCCTGGA¹CACCGTGTTCAGCACCAGCCTCAGAAGAGGCTCCTGCTCCGTCCGGGCACA¹ (960)
 280 PROPROGLYHISARGVALGLNHISGLNPROGLNLYSARGPROPROALAPROSERGLYTHR

FIG. 2A

Conty
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300 CAAGTTCAC¹CAGCAGAAAG²CCCCCCCCT³CCCCAGACCT⁴CGAGTTCAGC⁵AAAACCTCC⁶ (1020)
GLNVALHISGLNGLNLYSGLYPROPROLEU⁷PROARGPROARGVALGLNPROLYSPROPRO
320 CATGGGGCAGCAGAA⁸ACTCATTGTCCCCTTCCTCTAATTAAAAAAGATAGAAACTGTCT⁹ (1080)
HISGLYALAALAGLUASNSERLEUSERPRO¹⁰SERSERASNE¹¹ND
TTTTCAATAAAAAGCACTGTGGATTTCTGCCCTCCTGATGTGCATATCCGTACTTCCATG¹² (1140)
AGGTGTTTTCTGTGTGCAGAACATTGTCACTCCTGAGGCTGTGGGCCACAGCCACCTCT¹³ (1200)
GCATCTTCGAACTCAGCCATGTGGTCAACATCTGGAGTTTTTGGTCTCCTCAGAGAGCTC¹⁴ (1260)
CATCACACCAGTAAGGAGAAGCAATATAAGTGTGATTGCAAGAATGGTAGAGGACCGAGC¹⁵ (1320)
ACAGAAATCTTAGAGATTTCTTGTCCCCTCTCAGGTCATGTGTAGATGCCATAAATCAAG¹⁶ (1380)
TGATTGGTGTGCCTGGGTCTCACTACAAGCAGCCTATCTGCTTAAGAGACTCTGGAGTTT¹⁷ (1440)
CTTATGTGCCCTGGTGGACACTTGCCACCATCCTGTGAGTAAAGTGAATAAAAGCTT¹⁸ (1500)
TGAC (1504)

FIG. 2B

1 GCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT
 51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAAGTGGCT
 101 TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA
 151 GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT
 201 AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG
 251 GGTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA
 301 ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA
 351 ACTGAGATAC CTACAGCGTG AGCATTGAGA AAGCGCCACG CTTCCCGAAG
 401 GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG
 451 CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT
 501 CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTGTGA TGCTCGTCAG
 551 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCAAGCTA GCTTCTAGCT
 601 AGAAATTGTA AACGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTGT
 651 AAATCAGCTC ATTTTITAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT
 701 AAATCAAAG AATAGCCCGA GATAGGGTTG AGTGTTGTT CAGTTTGGAA
 751 CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAA GGGCGAAAAA
 801 CCGTCTATCA GGGCGATGGC CGCCCACTAC GTGAACCATC ACCCAAATCA
 851 AGTTTTTTGG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG
 901 GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA
 951 AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA
 1001 GCGGTCACGC TGCGCGTAAC CACCACACC GCCGCGCTTA ATGCGCGCT
 1051 ACAGGGCGCG TACTATGGTT GCTTTGACGA GCACGTATAA CGTGCTTTCC

FIG. 6A

1101 TCGTTGGAAT CAGAGCGGGA GCTAAACAGG AGGCCGATTA AAGGGATTTT
 1151 AGACAGGAAC GGTACGCCAG CTGGATCACC GCGGTCTTTC TCAACGTAAC
 1201 ACTTTACAGC GGCGCGTCAT TTGATATGAT GCGCCCCGCT TCCCCATAAG
 1251 GGAGCAGGCC AGTAAAAGCA TTACCCGTGG TGGGGTCCC GAGCGGCCAA
 1301 AGGGAGCAGA CTCTAAATCT GCCGTCATCG ACTTCGAAGG TTCGAATCCT
 1351 TCCCCACCA CCATCACTTT CAAAAGTCCG AAAGAATCTG CTCCTGCTT
 1401 GTGTGTTGGA GGTCGCTGAG TAGTGCGCGA GTAAAATTTA AGCTACAACA
 1451 AGGCAAGGCT TGACCGACAA TTGCATGAAG AATCTGCTTA GGGTTAGGCG
 1501 TTTTGGCTG CTTGCGGATG TACGGGCCAG ATATACGCGT TGACATTGAT
 1551 TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC
 1601 CCATATATGG AGTTCCGCGT TACATAACTT ACGGTAAATG GCGCGCCTGG
 1651 CTGACCGCCC AACGACCCCC GCCCATTGAC GTCAATAATG ACGTATGTTC
 1701 CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGACTAT
 1751 TTACGGTAAA CTGCCCACTT GGCAGTACAT CAAGTGTATC ATATGCCAAG
 1801 TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCGCC TGGCATTATG
 1851 CCCAGTACAT GACCTTATGG GACTTTCCTA CTTGGCAGTA CATCTACGTA
 1901 TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG
 1951 GCGTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATTG
 2001 ACGTCAATGG GAGTTTGTTT TGGCACCAA ATCAACGGGA CTTTCCAAAA
 2051 TGTGTAACA ACTCCGCCCC ATTGACGCAA ATGGCGGAA TTCCTGGGCG
 2101 GGA CTGGGGA GTGGCGAGCC CTCAGATGCT GCATATAAGC AGCTGCTTTT
 2151 TGCCTGTA CT GGGTCTCTCT GGTTAGACCA GATCTGAGCC TGGGAGCTCT
 2201 CTGGCTAACT AGAGAACCCA CTGCTTAAGC CTCAATAAAG CTTCTAGAGA
 2251 TCCCTCGACC TCGAGATCCA TTGTGCTGGC GCGGATTCTT TATCACTGAT

FIG. 6B

2301 AAGTTGGTGG ACATATTATG TTTATCAGTG ATAAAGTGTC AAGCATGACA
 2351 AAGTTGCAGC CGAATACAGT GATCCGTGCC GCCCTAGACC TGTTGAACGA
 2401 GGTCCGGCGTA GACGGTCTGA CGACACGCAA ACTGGCGGAA CGGTTGGGGG
 2451 TTCAGCAGCC GGCGCTTTAC TGGCACTTCA GGAACAAGCG GGCGCTGCTC
 2501 GACGCACTGG CCGAAGCCAT GCTGGCGGAG AATCATAGCA CTTCGGTGCC
 2551 GAGAGCCGAC GACGACTGGC GCTCATTCT GACTGGGAAT GCGCGCAGCT
 2601 TCAGGCAGGC GCTGCTCGCC TACCGCCAGC ACAATGGATC TCGAGGGATC
 2651 TTCCATACCT ACCAGTTCTG CGCCTGCAGG TCGCGGCCGC GACTCTAGAG
 2701 GATCTTTGTG AAGGAACCTT ACTTCTGTGG TGTGACATAA TTGGACAAAC
 2751 TACCTACAGA GATTTAAAGC TCTAAGGTAA ATATAAAATT TTTAAGTGTA
 2801 TAATGTGTTA AACTACTGAT TCTAATTGTT TGTGTATTTT AGATTCCAAC
 2851 CTATGGAAC~~T~~GATGAATGGG AGCAGTGGTG GAATGCCTTT AATGAGGAAA
 2901 ACCTGTTTTG CTCAGAAGAA ATGCCATCTA GTGATGATGA GGCTACTGCT
 2951 GACTCTCAAC ATTCTACTCC TCCAAAAAAG AAGAGAAAGG TAGAAGACCC
 3001 CAAGGACTTT CCTTCAGAAT TGCTAAGTTT TTTGAGTCAT GCTGTGTTTA
 3051 GTAATAGAAC TCTTGCTTGC TTTGCTATTT ACACCACAAA GGAAAAAGCT
 3101 GCACTGCTAT ACAAGAAAAT TATGGAAAAA TATTCTGTAA CCTTTATAAG
 3151 TAGGCATAAC AGTTATAATC ATAACATACT GTTTTTTCTT ACTCCACACA
 3201 GGCATAGAGT GTCTGCTATT AATAACTATG CTCAAAAATT GTGTACCTTT
 3251 AGCTTTTTTAA TTTGTAAAGG GGTTAATAAG GAATATTTGA TGTATAGTGC
 3301 CTTGACTAGA GATCATAATC AGCCATACCA CATTTGTAGA GGTTTTACTT
 3351 GCTTTAAAAA ACCTCCCACA CCTCCCCCTG AACCTGAAAC ATAAAATGAA
 3401 TGCAATTGTT GTTGTTAACT TGTTTATTGC AGCTTATAAT GGTTACAAAT
 3451 AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TTTACTGCAT

FIG. 6C

3501 TCTAGTTGTG GTTTGTCCAA ACTCATCAAT GTATCTTATC ATGTCTGGAT
3551 CCTGTGGAAT GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG
3601 CAGGCAGAAG TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT
3651 GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT
3701 CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC
3751 TAACTCCGCC CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT
3801 TTTATTTATG CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA
3851 GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG CTTTGTGAAA AAGCTAATTC

FIG. 6D

AGACTCTCAGGCCTTGGCAGGTGCGTCTTTCAGTTCCTCCCTCACACTTCGGGTTCCTCGG (60)
 GAGGAGGGGCTGGAACCCTAGCCCATCGTCAGGACAAAGATGCTCAGGCTGCTCTTGGCT (120)
 METLEUARGLEULEULEALA
 -18
 CTCAACTTATTCCTTCAATTCAAGTAACAGGAAACAAGATTTTGGTGAAGCAGTCGCC (180)
 LEUASNLEUPHEPROSERILEGLNVALTHRGLYASNLYSILELEUVALLYSGLNSEPR
 +1
 ATGCTTGTAGCGTACGACAATGCGGTCAACCTTAGCTGCAGTATTCCTACAATCTCTTC (240)
 10 METLEUVALALATYRASPASNALAVASNLEUSERCYSLYSTYRSERTYRASNLEUPHE
 ---CHO---
 TCAAGGGAGTTCGGGCATCCCTTACAAAGGACTGGATAGTGCTGTGGAGTCTGTGT (300)
 30 SERARGGLUPHEARGALASERLEUHSLSGLYLEUASPSEALAVAGLUVALCYSVAL
 GTATATGGGAATTACTCCCAGCAGCTTCAGGTTTACTCAAAAACGGGGTCAACTGTGAT (360)
 50 VALTYRGLYASNTYRSEGLNGLNLEUGLNVALTYRSELYSTHRLYPHEASNCYSASP
 ---CHO---
 GGGAAATTGGGCAATGAATCAGTGACATTCTACCTCCAGATTTGTATGTTAACCAACA (420)
 70 GLYLYSLEUGLYASNGLUSERVALTHRPHETYLEUGLNASNLEUTYRVALASNGLNTHR
 ---CHO---
 GATATTTACTTCTGCAAAATTGAAGTTATGTATCCTCCTTACCTAGACAATGAGAAG (480)
 90 ASPILETYRPHECYSLYSILEGLUVALMETTYRPROPROTYRLEUASPASNGLULYS
 AGCAATGGAACCATTATCCATGTGAAAGGAAACACCTTTGTCCAAGTCCCCTATTCCC (540)
 110 SERASNGLYTHRILEILEHISVALLYSGLYLYSHISLEUCYSPROSERPROLEUPHEPRO
 ---CHO---
 GGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTGGTGGAGTCTGGCTTGCTATAGC (600)
 130 GLYPROSERLYSPROPHETRPVALLEUVALVALGLYGLYVALLEUALACYSYRSE
 ---TM---
 TTGCTAGTAACAGTGGCCTTTATTATTTCTGGGTGAGGAGTAAGAGGAGCAGGCTCTG (660)
 150 LEULEUVALTHRVALALAPHEILEILEPHETRPVALARGSERLYSARGSERARGLEULEU
 CACAGTGACTACATGAACATGACTCCCCGCCGCCCGGGCCACCCGCAAGCATTACCAG (720)
 170 HISSERASPTYRMETASNMETTHRPROARGARGPROGLYPROTHRARGLYSHISTYRGLN
 CCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCTGACACGGACGCCTATCCAG (780)
 190 PROTYRALAPROPROARGASPPHEALAALATYRARGSEREND
 202
 AGCCAGCCGGCTGGCAGCCCCCATCTGCTCAATATCACTGCTCTGGATAGGAAATGACCG (840)
 CCATCTCCAGCCGGCCACCTCAGCCCCTGTGGGCCACCAATGCCAATTTTCTCGAGTG (900)
 ACTAGACCAATATCAAGATCATTTTGAGACTCTGAAATGAAGTAAAGAGATTTCCTGT (960)
 GACAGGCCAAGTCTTACAGTGCATGGCCCACATTCCAACCTACCATGTACTTAGTGACT (1020)
 TGACTGAGAAGTTAGGGTAGAAAACAAAAAGGGAGTGAATTCTGGGAGCCTCTTCCCTTT (1080)

FIG. 7A

CTCACTCACCTGCACATCTCAGTCAAGCAAAGTGTGGTATCCACAGACATTTTAGTTGCA (1140)
GAAGAAAGGCTAGGAAATCATTCCCTTTTGGTTAAATGGGTGTTAATCTTTGGTTAGTG (1200)
GGTTAAACGGGGTAAGTTAGAGTAGGGGAGGGATAGGAAGACATATTAAAAACCATT (1260)
AAACACTGTCTCCCACTCATGAAATGAGCCACGTAGTTCCTATTTAATGCTGTTTTCTT (1320)
TAGTTTAAATACATAGACATTGTCTTTTATGAATTCTGATCATTTTAGTCATTTTGA (1380)
CCAAATGAGGGATTTGGTCAAATGAGGGAATCCCTCAAAGCAATATCAGGTAAACCAAGT (1440)
TGCTTTCCTCACTCCCTGTATGAGACTTCAGTGTTAATGTTACAATATACTTTGAAA (1500)
GAATAAAATAGTTC (1514)

FIG. 7B

TAGACCCAGAGAGGCTCAGCTGCACTCGCCCGGCTGGGAGAGCTGGGTGTGGGGAACATG (60)
 MET
 GCCGGGCCTCCGAGGCTCCTGCTGCTGCCCTGCTTCTGGCGCTGGCTCGCGGCCTGCCT (120)
 ALAGLYPROPROARGLEULEULEULEUPROLEULEULEUALALEUALAARGGLYLEUPRO
 GGGGCCCTGGCTGCCAAGGTAAGAGCTTCCCAGGCTCTCCATGGCCACAGCTCCGGAGC (180)
 GLYALALEUALAALAGLN /
 TCTCCCTGCCCATGAGCTCAGAGCCCCAGTCTGAGCCACAGCACAGCCCCAGGAAGC (240)
 GGGTGGGGTGTCTGAGCGGCCTCCAGTGTCTGAGGACTCAITTAAGAGAAGGAAAAAGGGT (300)
 GGACCCGGTGGGAGTGGCCGGGGCTGTCCAGGCAGGGCCGCTGCTTTGGGAGGAAGAAG (360)
 CCCACAGTCTCGGAACAGGAGACAGCACCTCCCCAACACCACAGCCGGTGGCCAGATC (420)
 TGCTCCATGCCCGTAAGGCACCGTGTCTTTGGCGACATGTCAGCCCTGGGCTGTCTCAG (480)
 GGCCCCACCATCCCCACCACTGTCCCCTGCAGGGAGGACATTCTGTCTTCTGGCCAG (540)
 ACTGATGGTGACAGCCCAGGTCTCCAGAGGTGCAGCAGTCTCCCCTGCACGACTGT (600)
 GLUVALGLNGLNSERPROHISCYSTHRTHRVA
 CCCCCTGGGAGCCTCCGTCAACATCACCTGCTCCACCAGCGGGGGCCTGCGTGGGATCTA (660)
 LPROVALGLYALASERVALASNILETHRCYSSERTHRSEGLYGLYLEUARGGLYLETY
 ---CHO---
 CCTGAGGCAGCTCGGGCCACAGCCCCAAGACATATTTACTACGAGGACGGGGTGGTGCC (720)
 RLEUARGGLNLEUGLYPROGLNPROGLNASPILEILETYRTYRGLUASPGLYVALVALPR
 CACTACGGAACAGACGGTTCGGGGCCGCACTGACTTCTCAGGGTCCCAGGACAACCTGAC (780)
 OTHRTHRASPARGARGPHEARGGLYARGILEASPPHESERGLYSERGLNASPASNLEUTH
 ---CHO---
 TATCACCATGCACCGCTGCAGCTGTCCGACTGGCACCTACACCTGCCAGGCCATCAC (840)
 RILETHRMETHISARGLEUGLNLEUSERASPTHRLYTHRTYRTHRCYGLNALAILETH
 -
 GGAGGTCAATGTCTACGGCTCCGGCACCCCTGGTCTGGTGACAGAGGAACAGTCCCAAGG (900)
 RGLUVALASNVALTYRGLYSERGLYTHRLEUVALLEUVALTHRGLUGLUGLNSERGLNGL
 ATGGCACAGATGCTCGGACGCCCCACCAAGGGCCTCTGCCCTCCCTGCCCCACCGACAGG (960)
 YTRPHISARGCYSSERASPALAPROPROARGALASERALEUPROALAPROPROTHRGL
 CTCCGCCCTCCCTGACCCGACAGACAGCCTCTGCCCTCCCTGACCCGCCAGCAGCCTCTGC (1020)
 YSERALEUPROASPPROGLNTHRALASERALEUPROASPPOPROALAALASERALE
 CCTCCCTGCGGCCCTGGCGGTGATCTCCTCCTCCTCGGCTGGGCCTGGGGGTGGCGTG (1080)
 ALEUPROALAALALEUALAVALILESERPHEULEUGLYLEUGLYLEUGLYVALALACY
 -----TM-----*

FIG. 8A

TGTGCTGGCGAGGACACAGATAAAGAACTGTGCTCGTGGCGGGATAAGAATTCGGCGGC (1140)
 SVALLEUALAARGTHRGLNILELYSLYSLEUCYSSERTRPARGASPLYSASNSERALAAL

 ATGTGTGGTGTACGAGGACATGTGCGACAGCCGCTGCAACACGCTGTCTCCCCCAACCA (1200)
 ACYSVALVALTYRGLUASP⁴⁴METSERHISSE⁴⁵RARGCYSASNTHRLEUSERSERPROAS⁴⁶NGL
 GTACCA⁴⁷GTGACCCAGTGGGCCCCTGCACGTCCCGCCTGTGGTCCCCCA⁴⁸GCACCTTCCCT (1260)
 NTYRGLNEND
 GCCCCACCA⁴⁹TGCCCCCACCCTGCCACACCCCTCACCTGTCTCTCCACGGCTGCA⁵⁰ (1320)
 CAGAGTTTG⁵¹AAGGGCCCAGCEGTGCCAGCTCCAAGCAGACACACAGGCAGTGGCCAGGC (1380)
 CCCACGGTGCTTCTCAGTGGACAATGATGCCTCTCCGGGAAGCCTTCCCTGCCCA⁵²AGCC (1440)
 ACGCCGCCA⁵³CCGGGAGGAAGCCTGACTGTCTTTGGCTGCATCTCCCGA⁵⁴CCATGGCCAAG (1500)
 GAGGGCTTTTCTGTGGGATGGGCCTGGCA⁵⁵CGCGCCCTCTCCTGTCA⁵⁶GTGCCGGCCAC⁵⁷C (1560)
 CACCAGCAG⁵⁸CCCCCAACCC⁵⁹CCAGGCAGC⁶⁰CGGCAGAG⁶¹ACGGGAGGAG⁶²ACCAGTCCCC⁶³C (1620)
 ACCCAGCCGTACCAGAAATAAAGGCTTCTGTGCTTCAAAAA⁶⁴AAAAA (1665)

FIG. 8B

CCCAAATGTCTCAGAATGTATGTCCAGAAACCTGTGGCTGCTTCAACCATTGACAGTTT (60)
 METSERGLNASNVALCYSPROARGASNLEUTRPLEULEUGLNPROLEUTHRVALL
 -29
 TGCTGCTGCTGGCTTCTGCAGACAGTCAAGCTGCAGCTCCCCAAAGGCTGTGCTGAAAC (120)
 EULEULEULEUALASERALAASPSEGLNALAALAALAPROPROLYSALAVALLEULYS
 -1 +1
 TTGAGCCCCCGTGGATCAACGTGCTCCAGGAGGACTCTGTGACTCTGACATGCCAGGGGG (180)
 10 EUGLUPROPROTRPILEASNVALLEUGLNGLUASPSERVALTHRLEUTHRCYSGLNGLYA
 *
 CTCGCAGCCCTGAGAGCGACTCCATTCACTGGTTCACAATGGGAATCTCATTCCCACC (240)
 30 LAARGSERPROGLUSERASPSERILEGLNTRPPHEHISASNGLYASNLEUILEPROTHR
 *
 ACACGCAGCCAGCTACAGGTTCAAGGCCACAACAATGACAGCGGGGAGTACACGTGCC (300)
 50 ISTHRGLNPROSERTYRARGPHELYSALAASNASNASNASPSERGLYGLUTYRTHRCYS
 ---CHO---
 *
 AGACTGGCCAGACCAGCCTCAGCGACCCTGTGCATCTGACTGTGCTTTCCGAATGGCTGG (360)
 70 LNTHRGlyGLNTHRSERLEUSERASPPROVALHISLEUTHRVALLEUSERGLUTRPLEUV
 *
 TGCTCCAGACCCCTCACCTGGAGTTCCAGGAGGGAGAAACCATCATGCTGAGGTGCCACA (420)
 90 ALLEUGLNTHRPROHISLEUGLUPHEGLNGLUGLYGLUTHRILEMETLEUARGCYSHISS
 *
 GCTGGAAGGACAAGCCTCTGGTCAAGGTCAATTCTTCCAGAATGGAAAATCCCAGAAAT (480)
 110 ERTPLYSASPLYSPOLEUVALLYVALTHRPHEPHEGLNASNGLYLYSSERGLNLYSP
 *
 TCTCCGTTTGGATCCACCTTCTCCATCCACAAGCAAACCACAGTCAAGTGGTGATT (540)
 130 HESERARGLEUASPPROTHRPHESERILEPROGLNALAASNHISSEHISSEGLYASPT
 ---CHO---
 *
 ACCACTGCAACAGGAAACATAGGCTACAGCTGTTCTCATCCAAGCCTGTGACCATCACTG (600)
 150 YRHISCYSTHRGLYASNILEGLYTYRTHRLEUPHESERSELYSPROVALTHRILETHRV
 *
 TCCAAGTGCCAGCATGGGCAGCTCTTCAACCAATGGGATCATTGTGGCTGTGGTCATTG (660)
 170 ALGLNVALPROSERMETGLYSERSESERPROMETGLYILEILEVALALAVALLILEA
 *
 CGACTGCTGTAGCAGCCATTGTTGCTGCTGTAGTGGCCTTGATCTACTGCAGGAAAAAGC (720)
 190 LATHRALAVALLAALAILEVALALAALAVALVALALEUILEYRCYSARGLYSLYSA
 -----TM-----
 *
 GGATTTGAGCCAATTCAGTATCCTGTGAAGGCTGCCAATTTGAGCCACCTGGACGTC (780)
 210 RGILESERALAASNSETRHASPPOVALLYSALAALAGLNPHEGLUPROPROGLYARGG
 *
 AAATGATTGCCATCAGAAAGAGACAACCTGAAGAAACCAACAATGACTATGAAACAGCTG (840)
 230 LNMETILEALAILEARGLYSARGGLNLEUGLUGLUTHRASNASNASPTYRGLUTHRALAA
 *
 ACGCGGCTACATGACTCTGAACCCAGGGCACCTACTGACGATGATAAAAACATCTACC (900)
 250 SPGLYGLYTYRMETTHRLEUASNPROARGALAPROTHRASPASPASPLYSASNILETYRL

FIG. 9-A

1 CTCAGCCTCGCTATGGCTCCCAGCAGCCCCCGCGCTGCCCGCACCTCTGGTCCTCGGGGCTCTGTTCCTCCCA
MetAlaProSerSerProArgProAlaLeuProAlaLeuLeuValLeuLeuGlyAlaLeuPhePro
(-25)
GGACCTGGCAATGCCCCAGACATCTGTGTCCCCCTCAAAAGTC
GlyProGlyAsnAlaGlnThrSerValSerProSerLysVal
(+11)
121 ATCTGCCCCGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCCAAGTTGTTGGGCATAGAGACC
IleLeuProArgGlyGlySerValLeuValThrCysSerThrSerCysAspGlnProLysLeuLeuGlyIleGluThr
(+1)
CCGTTGCCTAAAAAGGAGTTGCTCCTGCCTGGGGAACAACCGG
ProLeuProLysLysGluLeuLeuLeuProGlyAsnAsnArg
(+51)
241 AAGGTGTATGAAGTGAAGCAATGTGCAAGAAAGATAGCCAAACCAATGTGCTATTCAAACCTGCCCTGATGGGCAGTCAACA
LysValTyrGluLeuSerAsnValGlnGluAspSerGlnProMetCysTyrSerAsnCysProAspGlyGlnSerThr
GCTAAACACCTTCCTCACCGTGTACTGGACTCCAGAACGGGTG
AlaLysThrPheLeuThrValTyrTrpThrProGluArgVal
(+91)
361 GAACTGGCACCCCTCCCCCTCTTGGCAGCCAGTGGGCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGCACCC
GluLeuAlaProLeuProSerTrpGlnProValGlyLysAsnLeuThrLeuArgCysGlnValGluGlyGlyAlaPro
---CHO---
CGGGCCAAACCTCACCGTGGTGCTGCTCCGTGGGAGAGAAGAG
ArgAlaAsnLeuThrValValLeuLeuArgGlyGluLysGlu
-----(+131)
481 CTGAAACGGGAGCCAGCTGTGGGGAGCCCGCTGAGGTCACGACCACCGGTGCTGTGAGGAGAGATCACCATGGAGCC
LeuLysArgGluProAlaValGlyGluProAlaGluValThrThrValLeuValArgArgAspHisGlyAla
AATTTCTCGTGCCCGCACTGAACTGGACCTGCGGCCCCCAAGGG
AsnPheSerCysArgThrGluLeuAspLeuArgProGlnGly
---CHO---(+171)
601 CTGGAGCTGTTTGAGAACACCTCGGCCCCCTACCAGCTCCAGACCTTGTCTCTGCCAGCGACTCCCCCACAACCTTGTC
LeuGluLeuPheGluAsnThrSerAlaProTyrGlnLeuGlnThrPheValLeuProAlaThrProProGlnLeuVal
---CHO---
AGCCCCCGGCTCCTAGAGGTGGACACGACGGGACCGTGGTC
SerProArgValLeuGluValAspThrGlnGlyThrValVal
(+211)

FIG. 11-A

721 TGTTCCTGGACGGGCTGTTCCAGTCTCGGAGGCCAGGTCCACCTGGCAGTGGGGACAGAGGTTGAACCCACACA
 CysSerLeuAspGlyLeuPheProValSerGluAlaGlnValHisLeuAlaLeuGlyAspGlnArgLeuAsnProThr
 GTCACCTATGGCAACGACTCCTTCTCGGCCAAGGCCCTCAGTC
 ValThrTyrGlyAsnAspSerPheSerAlaLysAlaSerVal
 (+251)
 ---CHO---
 841 AGTGTGACCGCAGAGGACGAGGGCACCCAGCGGCTGACGTGTGCAGTAATACTGGGGAACAGAGCCAGGAGACACTG
 SerValThrAlaGluAspGluGlyThrGlnArgLeuThrCysAlaValIleLeuGlyAsnGlnSerGlnGluThrLeu
 ---CHO---
 CAGACAGTGACCATCTACAGCTTTCGGGCGCCCAACGTGATT
 GlnThrValThrIleTyrSerPheProAlaProAsnValIle
 (+291)
 961 CTGACGAAGCCAGAGGTCTCAGAAAGGACCGAGGTGACAGTGAAGTGTGAGGCCACCCCTAGAGCCAAAGGTGACGCTG
 LeuThrLysProGluValSerGluGlyThrGluValThrValLysCysGluAlaHisProArgAlaLysValThrLeu
 AATGGGTTCCAGCCAGCCACTGGGCCCGAGGGCCCCAGCTC
 AsnGlyValProAlaGlnProLeuGlyProArgAlaGlnLeu
 (+331)
 1081 CTGCTGAAGGCCACCCAGAGGACAAACGGCGCAGCTTCTCCTGCTCTGCAACCCTGGAGGTGGCCGGCCAGCTTATA
 LeuLeuLysAlaThrProGluAspAsnGlyArgSerPheSerCysSerAlaThrLeuGluValAlaGlyGlnLeuIle
 CACAAGAACCAGACCCGGAGCTTCGTGTCCTGTATGGCCCC
 HisLysAsnGlnThrArgGluLeuArgValLeuTyrGlyPro
 (+371)
 ---CHO---
 1201 CGACTGGACGAGGGGATTGTCCGGGAAACTGGACGTGGCCAGAAATTCCCAGCAGACTCCAATGTGCCAGGCTTGG
 ArgLeuAspGluArgAspCysProGlyAsnTrpThrTrpProGluAsnSerGlnThrProMetCysGlnAlaTrp
 ---CHO---
 GGGAAACCCATTGCCCCGAGCTCAAGTGTCTAAAGGATGGCACT
 GlyAsnProLeuProGluLeuLysCysLeuLysAspGlyThr
 (+411)
 1321 TTCCCACTGCCCATCGGGGAATCAGTGACTGTCACTCGAGATCTTGAGGGCACCTACCTCTGTGGGCCAGGAGCACT
 PheProLeuProIleGlyGluSerValThrValThrArgAspLeuGluGlyThrTyrLeuCysArgAlaArgSerThr
 CAAGGGAGGTCAACCCCGGAGGTGACCGTGAATGTGCTCTCC
 GlnGlyGluValThrArgGluValThrValAsnValLeuSer
 (+451)

FIG. 11-B

1441 CCCCCGTATGAGATTGTTCATCATCTGTTGGTAGCAGCCGCGAGTCATAATGGGCACTGCAGGCCCTCAGCACGTACCTC
ProArgTyrGluIleValIleIleThrValValAlaAlaValIleMetGlyThrAlaGlyLeuSerThrTyrLeu
-----TM-----
TATAACCGCCAGCGGAAGATCAAGAAATACAGACTACAACAG
TyrAsnArgGlnArgLysIleLysLysTyrArgLeuGlnGln
(+491)

1561 GCCCAAAAAGGGACCCCCCATGAAACCGAACACACAAGCCCTCCCTGAACCTATCCCCGGGACAGGGCCCTCTTCCT
AlaGlnLysGlyThrProMetLysProAsnThrGlnAlaThrProPro
(+507)
CGGCCCTTCCCATATTGGTGGCAGTGGTGCCACACTGAACAGA

1681 GTGGAAGACATATGCCCATGCCAGCTACACCTACCGGCCCTGGGACGCCCGGAGGACAGGGCATTGTCTCAGTCAGATAC
1801 GGCCACGCATCTGATCTGTAGTCACATGACTAAGCCCAAGAGGAAGG
AACAGCAATTGGGGCCCATGGTACCTGCACACCTAAACACTA

FIG. 11-C

1 ..GGAGAGTC TGACCACCAT GCCACCTCCT CGCCTCCTCT TCTTCCTCCT
 51 CTTCTCACC CCCATGGAAG TCAGGCCCGA GGAACCTCTA GTGGTGAAGG
 101 TGAAGAGGG AGATAACGCT GTGCTGCAGT GCCTCAAGGG GACCTCAGAT
 151 GGGCCCACTC AGCAGCTGAC CTGGTCTCGG GAGTCCCCGC TTAAACCCTT
 201 CTTAAAACTC AGCCTGGGGC TGCCAGGCCT GGAATCCAC ATGAGGCCCC
 251 TGGCCATCTG GCTTTTCATC TTCAACGTCT CTCAACAGAT GGGGGGCTTC
 301 TACCTGTGCC AGCCGGGGCC CCCCTCTGAG AAGGCCTGGC AGCCTGGCTG
 351 GACAGTCAAT GTGGAGGGCA GCGGGGAGCT GTTCCGGTGG AATGTTTCGG
 401 ACCTAGGTGG CCTGGGCTGT GGCCTGAAGA ACAGTCCTC AGAGGGCCCC
 451 AGCTCCCCCT CCGGAAGCT CATGAGCCCC AAGCTGTATG TGTGGGCCAA
 501 AGACCGCCCT GAGATCTGGG AGGGAGAGCC TCCGTGTGTC CCACCGAGGG
 551 ACAGCCTGAA CAGAGCCTC AGCCAGGACC TCACCATGGC CCCTGGCTCC
 601 ACACTCTGGC TGTCTGTGG GGTACCCCT GACTCTGTGT CCAGGGCCCC
 651 CCTCTCCTGG ACCCATGTGC ACCCAAGGG GCCTAAGTCA TTGCTGAGCC
 701 TAGAGCTGAA GGACGATCGC CCGGCCAGAG ATATGTGGGT AATGGAGACG
 751 GGTCTGTTGT TGCCCCGGGC CACAGCTCAA GACGCTGGAA AGTATTATTG
 801 TCACCGTGGC AACCTGACCA TGTCATTCCA CCTGGAGATC ACTGCTCGGC
 851 CAGTACTATG GCACTGGCTG CTGAGGACTG GTGGCTGGAA GGTCTCAGCT
 901 GTGACTTTGG CTTATCTGAT CTTCTGCCTG TGTTCCCTTG TGGGCATTCT
 951 TCATCTTCAA AGAGCCCTGG TCCTGAGGAG GAAAAGAAAG CGAATGACTG
 1001 ACCCCACCAG GAGATTCTTC AAAGTGACGC CTCCCCAGG AAGCGGGCCC
 1051 CAGAACCAGT ACGGGAACGT GCTGTCTCTC CCCACACCCA CCTCAGGCCT
 1101 CGGACGCGCC CAGCGTTGGG CCGCAGGCCT GGGGGGCACT GCCCCGTCTT
 1151 ATGGAAACCC GAGCAGCGAC GTCCAGGCGG ATGGAGCCTT GGGGTCCCGG

FIG. 12-A

1201 AGCCGCCGGG AGTGGGCCCCA GAAGAAGAGG AAGGGGAGGG CTATGAGGAA
1251 CCTGACAGTG AGGAGGACTC CGAGTTCTAT GAGAACGACT CCAACCTTGG
1301 GCAGGACCAG CTCTCCCAGG ATGGCAGCGG CTACGAGAAC CCTGAGGATG
1351 AGCCCCTGGG TCCTGAGGAT GAAGACTCCT TCTCCAACGC TGAGTCTTAT
1401 GAGAACGAGG ATGAAGAGCT GACCCAGCCG GTCGCCAGGA CAATGGACTT
1451 CCTGAGCCCT CATGGGTCAG CCTGGGACCC CAGCCGGGAA GCAACCTCCC
1501 TGGGGTCCCA GTCCTATGAG GATATGAGAG GAATCCTGTA TGCAGCCCCC
1551 CAGCTCCGCT CCATTTCGGG CCAGCCTGGA CCCAATCATG AGGAAGATGC
1601 AACTCTTAT GAGAACATGG ATAATCCCGA TGGGCCAGAC CCAGCCTGGG
1651 GAGGAGGGGG CCGCATGGGC ACCTGGAGCA CCAGGTGATC CTCAGGTGGC
1701 CAGCCTGGAT CTCCTCAAGT CCCCAAGATT CACACCTGAC TCTGAAATCT
1751 GAAGACCTCG AGCAGATGAT GCCAACCTCT GGAGCAATGT TGCTTAGGAT
1801 GTGTGCATGT GTGTAAGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT
1851 ATACATGCCA GTGACACTTC CAGTCCCCTT TGTATTCCTT AAATAAACTC
1901 AATGAGCTCT TCCAAAAAAA AAAA

FIG. 12-B

1 ACAAAGACAA ACTGCACCCA CTGAACTCCG CAGCTAGCAT CCAAATCAGC
51 CCTTGAGATT TGAGGCCTTG GAGACTCAGG AGTTTTGAGA GCAAAATGAC
101 AACACCCAGA AATTCAGTAA ATGGGACTTT CCCGGCAGAG CCAATGAAAG
151 GCCCTATTGC TATGCAATCT GGTCCAAAAC CACTCTTCAG GAGGATGTCT
201 TCACTGGTGG GCCCCACGCA AAGCTTCTTC ATGAGGGAAT CTAAGACTTT
251 GGGGGCTGTC CAGATTATGA ATGGGCTCTT CCACATTGCC CTGGGGGGTC
301 TTCTGATGAT CCCAGCAGGG ATCTATGCAC CCATCTGTGT GACTGTGTGG
351 TACCCTCTCT GGGGAGGCAT TATGTATATT ATTTCCGGAT CACTCCTGGC
401 AGCAACGGAG AAAAATCCA GGAAGTGTTT GGTCAAAGGA AAAATGATAA
451 TGAATTCATT GAGCCTCTTT GCTGCCATTT CTGGAATGAT TCTTTCAATC
501 ATGGACATAC TTAATATTAA AATTTCCCAT TTTTAAAAA TGGAGAGTCT
551 GAATTTTATT AGAGCTCACA CACCATATAT TAACATATAC AACTGTGAAC
601 CAGCTAATCC CTCTGAGAAA AACTCCCCAT CTACCCAATA CTGTTACAGC
651 ATACAATCTC TGTTCTTGGG CATTTTGTCA GTGATGCTGA TCTTTGCCTT
701 CTTCCAGGAA CTTGTAATAG CTGGCATCGT TGAGAATGAA TGGAAAAGAA
751 CGTGCTCCAG ACCCAAATCT AACATAGTTC TCCTGTCAGC ACAAGAAAAA
801 AAAGAACAGA CTATTGAAAT AAAAGAAGAA GTGGTTGGGC TAACTGAAAC
851 ATCTTCCCAA CCAAAGAATG AAGAAGACAT TGAAATTATT CCAATCCAAG
901 AAGAGGAAGA AGAAGAAACA GAGACGAACT TTCCAGAACC TCCCCAAGAT
951 CAGGAATCCT CACCAATAGA AAATGACAGC TCTCCTTAAG TGATTTCTTC
1001 TGTTTTCTGT TTCCTTTTTT AAACATTAGT GTTCATAGCT TCCAAGAGAC
1051 ATGCTGACTT TCATTTCTTG AGGTACTCTG CACATACGCA CCACATCTCT

FIG. 13-A

1101 ATCTGGCCTT TGCATGGAGT GACCATAGCT CCTTCTCTCT TACATTGAAT
1151 GTAGAGAATG TAGCCATTGT AGCAGCTTGT GTTGTCACGC TTCTTCTTTT
1201 GAGCAACTTT CTTACACTGA AGAAAGGCAG AATGAGTGCT TCAGAATGTG
1251 ATTCCTACT AACCTGTTCC TTGGATAGGC TTTTATAGTAT AGTATTTTTT
1301 TTTGTCATTT TCTCCATCAG CAACCAGGGA GACTGCACCT GATGGAAAAG
1351 ATATATGACT GCTTCATGAC ATTCCTAAAC TATCTTTTTT TTATTCCACA
1401 TCTACGTTTT TGGTGGAGTC CCTTTTTATC ATCCTTAAAA CAATGATGCA
1451 AAAGGGCTTT AGAGCACAAT GGATCT

FIG. 13-B

1 CCCAAATGTC TCAGAATGTA TGTCCCAGAA ACCTGTGGCT GCTTCAACCA
51 TTGACAGTTT TGCTGCTGCT GGCTTCTGCA GACAGTCAAG CTGCAGCTCC
101 CCCAAAGGCT GTGCTGAAAC TTGAGCCCCC GTGGATCAAC GTGCTCCAGG
151 AGGACTCTGT GACTCTGACA TGCCAGGGGG CTCGCAGCCC TGAGAGCGAC
201 TCCATTCACT GGTTCACAA TGGGAATCTC ATTCCCACCC ACACGCAGCC
251 CAGCTACAGG TTCAAGGCCA ACAACAATGA CAGCGGGGAG TACACGTGCC
301 AGACTGGCCA GACCAGCCTC AGCGACCCTG TGCATCTGAC TGTGCTTTCC
351 GAATGGCTGG TGCTCCAGAC CCCTCACCTG GAGTTCCAGG AGGGAGAAAC
401 CATCATGCTG AGGTGCCACA GCTGGAAGGA CAAGCCTCTG GTCAAGGTCA
451 CATTCTTCCA GAATGGAAAA TCCCAGAAAT TCTCCCGTTT GGATCCCACC
501 TTCTCCATCC CACAAGCAAA CCACAGTCAC AGTGGTGATT ACCACTGCAC
551 AGGAAACATA GGCTACACGC TGTTCTCATC CAAGCCTGTG ACCATCACTG
601 TCCAAGTGCC CAGCATGGGC AGCTCTTAC CAATGGGGAT CATTGTGGCT
651 GTGGTCATTG CGACTGCTGT AGCAGCCATT GTTGCTGCTG TAGTGGCCTT
701 GATCTACTGC AGGAAAAAGC GGATTTACGC CAATTCCACT GATCCTGTGA
751 AGGCTGCCCCA ATTTGAGCCA CCTGGACGTC AAATGATTGC CATCAGAAAG
801 AGACAACCTG AAGAAACCAA CAATGACTAT GAAACAGCTG ACGGCGGCTA
851 CATGACTCTG AACCCCAGGG CACCTACTGA CGATGATAAA AACATCTACC
901 TGACTCTTCC TCCCAACGAC CATGTCAACA GTAATAACTA AAGAGTAACG
951 TTATGCCATG TGGTCATACT CTCAGCTTGC TGAGTGGATG AAAAAAGAG
1001 GGGAAATTGT AAAGGAAAAAT TTAAATGGAG ACTGGAAAAA TCCTGAGCAA
1051 AAAAAACCAC CTGGCCCTTA GAAATAGCTT TAACTTTGCT TAACTACAA
1101 ACACAAGCAA AACTTCACGG GGTCACTATA CATAAAGCA TAAGCAAAAC
1151 TTAACCTGGA TCATTTCTGG TAAATGCTTA TGTTAGAAAT AAGACAACCC
1201 CAGCCAATCA CAAGCAGCCT ACTAACATAT AATTAGGTGA CTAGGGACTT
1251 TCTAAGAAGA TACCTACCCC CAAAAACAA TTATGTAATT GAAAACCAAC
1301 CGATTGCCTT TATTTTGCTT CCACATTTTC CCAATAAATA CTTGCCTGTG
1351 ACATTTTGCC ACTGGAACAC TAAACTTCAT GAATTGCGCC TCAGATTTTT
1401 CCTTTAACAT CTTTTTTTTT TTTGACAGAG TCTCAATCTG TTACCCAGGC
1451 TGGAGTGCAG TGGTGCTATC TTGGCTCACT GCAAACCCGC CTCCCAGGTT
1501 TAAGCGATTG TCATGCCTCA GCCTCCCAGT AGCTGGGATT AGAGGCATGT
1551 GCCATCATAC CCAGCTAATT TTTGTATTTT TTATTTTTTT TTTTGTAGTAG
1601 AGACAGGGTT TCGCAATGTT GGCCAGGCCG ATCTCGAACT TCTGGCCTCT
1651 AGCGATCTGC CCGCCTCGGC CTCCCAAAGT GCTGGGATGA CCAGCATCAG

FIG. 14-A

1701 CCCCAATGTC CAGCCTCTTT AACATCTTCT TTCCTATGCC CTCTCTGTGG
1751 ATCCCTACTG CTGGTTTCTG CCTTCTCCAT GCTGAGAACA AAATCACCTA
1801 TTCACTGCTT ATGCAGTCGG AAGCTCCAGA AGAACAAGA GCCCAATTAC
1851 CAGAACCACA TTAAGTCTCC ATTGTTTTGC CTTGGGATTT GAGAAGAGAA
1901 TTAGAGAGGT GAGGATCTGG TATTCCTGG ACTAAATTCC CCTTGGGGAA
1951 GACGAAGGGA TGCTGCAGTT CCAAAAGAGA AGGACTCTTC CAGAGTCATC
2001 TACCTGAGTC CCAAAGCTCC CTGTCCTGAA AGCCACAGAC AATATGGTCC
2051 CAAATGACTG ACTGCACCTT CTGTGCCTCA GCCGTTCTTG ACATCAAGAA
2101 TCTTCTGTTT CACATCCACA CAGCCAATAC AATTAGTCAA ACCACTGTTA
2151 TTAACAGATG TAGCAACATG AGAAACGCTT ATGTTACAGG TTACATGAGA
2201 GCAATCATGT AAGTCTATAT GACTTCAGAA ATGTTAAAT AGACTAACCT
2251 CTAACAACAA ATTAAAAGTG ATTGTTTCAA GGTGAAAAA

FIG. 14-B

1 GCTGTGACTG CTGTGCTCTG GGCGCCACTC GCTCCAGGGA GTGATGGGAA
51 TCCTGTTCATT CTTACCTGTC CTTGCCACTG AGAGTGACTG GGCTGACTGC
101 AAGTCCCCC AGCCTTGGGG TCATATGCTT CTGTGGACAG CTGTGCTATC
151 CCTGGCTCCT GTTGCTGGGA CACCTGCAGC TCCCCAAAG GCTGTGCTGA
201 AACTCGAGCC CCAGTGGATC AACGTGCTCC AGGAGGACTC TGTGACTCTG
251 ACATGCCGGG GGA CTCACAG CCCTGAGAGC GACTCCATTC AGTGGTTCCA
301 CAATGGGAAT CTCATTCCCA CCCACACGCA GCCAGCTAC AGGTTCAAGG
351 CCAACAACAA TGACAGCGGG GAGTACACGT GCCAGACTGG CCAGACCAGC
401 CTCAGCGACC CTGTGCATCT GACTGTGCTT TCTGGTCAGT GGAGGAAGGC
451 CCCAGGGTGG ACCTGGGAGG GCCAGGACGG ATGAAATCTG CTTTCAGGCA
501 GAGGTTTGCA GGAAAGGGGG GTGGCCTGCT TACTGGGAAG TATCGCTGTG
551 AGTTGCCTCA GCACATATCA GTGGTTGTTT TTGCCTCAGT TCTGATTGAA
601 CAGAAGAAGG TTTCAAGGCC AAAACAGGC AGCCAAGTGT GAGAGAAGCA
651 GAAGGAAATC CCTACTGCAT AAAACCCATT TCCATTTTAA TGGCAGAATT
701 GAAAAGCACA GACCACA ACT GAATCCTAGC CCTGGAAATG ACTCACTATA
751 CAACATGATG AATTCATTTA ACCCTTGAGT TTCCATTTCT TCACCTGCTC
801 CGTGGGGCAG TAACGCCTCC CTCAGAGGCT TCTGGTGAGA ATCAGTGTTT
851 CCCTGCCCCC GCGCCGCCCT CCATGCCCCT TCTCCACGTT CTCACTGTGC
901 TAGGTGCTCT TCTCTGTCTT TCTCTTCCAC CAGCCTGTGG GAAACCTGAG
951 ATGAAAGTCG TGTCTTACCC ATCTTTGTAT TTCCAGCATC TGAAACTGGG
1001 CAGAGCTTAA TAAATATTTT GCTGGAGAGG TTGATGATCT TACAAAGCTC
1051 CCATTGAAAG GTGGCTCTCT GTAAAGCAAA GTTACAATGA GATTGTGATG
1101 AACATTGTCC TTGTGGCTTT TCACTTAGTC CCCTCCCTTC ACCTGAAGAG
1151 CAAATTTTCC TCAAAAGTAC ACAGCAAACG AATGACCCAC TGGTGACACT
1201 GTTGCCTTTA GACCCTGCTG GAAAGAAGCT CCACATTTAT TAACATTCCC
1251 GAAGTAAATT TATCAGGTAG CATTATCAG GTAACATTTG TTGCACATTC
1301 ATGACTTTTC TACTGTCCAC AAAGGCATAT GTCCTTATCA TATGCGGACT
1351 CCTCGGTCAC ACTGGATTCT TCCTTCCCTC CTCGACATGG AAGAGATGGC
1401 ATCTTAGGGT CTCTTGTTT CTTCTGCAG AGGCCTGTG GGCAGGAAAA
1451 GGCTGCAGCT GCCTTCCTGG GAGAAGGAGG AGATGAGTGT ATCCTGAACA
1501 CCTATTATGT GCTAGGGGCT ATTGTAGATA CATGACACTA TCATGCTCAT
1551 TTTACGAAT GAGGAACTG AGGCTCAGAA GACTTAAATT ATTTGCCCAA
1601 GAGTTATAAA TGACAGAGCC AGCATTAGAG TCCAGGACTG TCTGATTTC
1651 GACCTAAGCT GTTCCCTCTG CACATCGTGT CCCACCAGTA AGGAAGATCT

FIG. 15-A

1701 GGGTCTCAGA GCTGAGCCAA GACCTCCCGG GTCCTCTGCG GTTTTTTTGTG
1751 TCTTTCAGAG TGGCTGGTGC TCCAGACCCC TCACCTGGAG TTCCAGGAGG
1801 GAGAAACCAT CGTGCTGAGG TGCCACAGCT GGAAGGACAA GCCTCTGGTC
1851 AAGGTCACAT TCTTCCAGAA TGGAAAATCC AAGAAATTTT CCCGTTCCGA
1901 TCCCAACTTC TCCATCCCAC AAGCAAACCA CAGTCACAGT GGTGATTACC
1951 ACTGCACAGG AAACATAGGC TACACGCTGT ACTCATCCAA GCCTGTGACC
2001 ATCACTGTCC AAGCTCCCAG CTCTTCACCG ATGGGGATCA TTGTGGCTGT
2051 GGTCACGGG ATTGCTGTAG CGGCCATTGT TGCTGCTGTA GTGGCCTTGA
2101 TCTACTGCAG GAAAAAGCGG ATTTCAAGTT TGTAGCTCCT CCCGGTCCCT
2151 TTTGTTATCA GTTCCACTT T

FIG. 15-B

1 GCCTCGCTCG GCGGCCAGT GGTCTGCGG CCTGGTCTCA CCTCGCCATG
 51 GTTCGTCTGC CTCTGCAGTG CGTCCTCTGG GGCTGCTTGC TGACCGCTGT
 101 CCATCCAGAA CCACCCACTG CATGCAGAGA AAAACAGTAC CTAATAAACA
 151 GTCAGTGCTG TTCTTGTGTC CAGCCAGGAC AGAAACTGGT GAGTGACTGC
 201 ACAGAGTTCA CTGAAACGGA ATGCCTTCCT TGCGGTGAAA GCGAATTCCT
 251 AGACACCTGG AACAGAGAGA CACACTGCCA CCAGCACAAA TACTGCGACC
 301 CCAACCTAGG GCTTCGGGTC CAGCAGAAGG GCACCTCAGA AACAGACACC
 351 ATCTGCACCT GTGAAGAAGG CTGGCACTGT ACGAGTGAGG CCTGTGAGAG
 401 CTGTGTCTTG CACCGCTCAT GCTCGCCCGG CTTTGGGGTC AAGCAGATTG
 451 CTACAGGGGT TTCTGATACC ATCTGCGAGC CCTGCCCAGT CGGCTTCTTC
 501 TCCAATGTGT CATCTGCTTT CGAAAAATGT CACCCTTGGA CAAGCTGTGA
 551 GACCAAAGAC CTGGTTGTGC AACAGGCAGGC ACAAACAAGA CTGATGTTGT
 601 CTGTGGTCCC CAGGATCGGC TGAGAGCCCT GGTGGTGATC CCCATCATCT
 651 TCGGGATCCT GTTTGCCATC CTCTTGGTGC TGGTCTTTAT CAAAAAGGTG
 701 GCCAAGAAGC CAACCAATAA GGCCCCCAC CCCAAGCAGG AACCCAGGA
 751 GATCAATTTT CCCGACGATC TTCTGGGCTC CAACACTGCT GCTCCAGTGC
 801 AGGAGACTTT ACATGGATGC CAACCGGTCA CCCAGGAGGA TGGCAAAGAG
 851 AGTCGCATCT CAGTGCAGGA GAGACAGTGA GGCTGCACCC ACCCAGGAGT
 901 GTGGCCACGT GGGCAAACAG GCAGTTGGCC AGAGAGCCTG GTGCTGCTGC
 951 TGCAGGGGTG CAGGCAGAAG CGGGGAGCTA TGCCCACTCA GTGCCAGCCC
 CTC

FIG. 16